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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/782,980DATE: 03/12/2001
TIME: 10:21:57Input Set : A:\seqlist.txt
Output Set: N:\CRF3\03122001\I782980.raw

P.5

3 <110> APPLICANT: Khodadoust, Mehran M.
 4 MacBeth, Kyle J.
 5 Busfield, Samantha J.
 6 McCarthy, Sean A.
 7 Holtzman, Douglas A.
 8 Gu, Wei
 9 White, David
 10 Pan, Yang
 12 <120> TITLE OF INVENTION: NOVEL ITALY, LOR-2, STRIFE, TRASH, BDSF, LRSG, AND
 13 STMST PROTEIN AND NUCLEIC ACID MOLECULES AND USES
 14 THEREFOR
 16 <130> FILE REFERENCE: MNI-121CP
 C--> 18 <140> CURRENT APPLICATION NUMBER: US/09/782,980
 C--> 19 <141> CURRENT FILING DATE: 2001-02-13
 21 <150> PRIOR APPLICATION NUMBER: PCT/US00/02125
 22 <151> PRIOR FILING DATE: 2000-01-27
 24 <150> PRIOR APPLICATION NUMBER: 09/448,076
 25 <151> PRIOR FILING DATE: 1999-11-23
 27 <150> PRIOR APPLICATION NUMBER: 09/276,400
 28 <151> PRIOR FILING DATE: 1999-03-25
 30 <150> PRIOR APPLICATION NUMBER: 60/117,580
 31 <151> PRIOR FILING DATE: 1999-01-27
 33 <150> PRIOR APPLICATION NUMBER: 09/014,195
 34 <151> PRIOR FILING DATE: 1998-01-27
 36 <150> PRIOR APPLICATION NUMBER: 09/014,348
 37 <151> PRIOR FILING DATE: 1998-01-27
 39 <150> PRIOR APPLICATION NUMBER: 09/086,892
 40 <151> PRIOR FILING DATE: 1998-05-29
 42 <150> PRIOR APPLICATION NUMBER: 09/296,208
 43 <151> PRIOR FILING DATE: 1999-04-21
 45 <150> PRIOR APPLICATION NUMBER: 09/063,950
 46 <151> PRIOR FILING DATE: 1998-04-21
 48 <150> PRIOR APPLICATION NUMBER: 09/561,381
 49 <151> PRIOR FILING DATE: 2000-04-28
 51 <150> PRIOR APPLICATION NUMBER: 09/561,810
 52 <151> PRIOR FILING DATE: 2000-04-28
 54 <150> PRIOR APPLICATION NUMBER: 09/087,121
 55 <151> PRIOR FILING DATE: 1998-05-29
 57 <150> PRIOR APPLICATION NUMBER: 09/672,721
 58 <151> PRIOR FILING DATE: 2000-09-28
 60 <150> PRIOR APPLICATION NUMBER: 09/049,799
 61 <151> PRIOR FILING DATE: 1998-03-27
 63 <160> NUMBER OF SEQ ID NOS: 176
 65 <170> SOFTWARE: PatentIn Ver. 2.0
 67 <210> SEQ ID NO: 1
 68 <211> LENGTH: 991
 69 <212> TYPE: DNA

ENTERED

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70 <213> ORGANISM: Homo sapiens
72 <220> FEATURE:
73 <221> NAME/KEY: CDS
74 <222> LOCATION: (43)..(573)
76 <400> SEQUENCE: 1
77 gaattccgac aaggagcagc ccgcaagcac caagtgagag gc atg aag tta cag      54
78                                     Met Lys Leu Gln
79                                     1
81 tgt gtt tcc ctt tgg ctg ggt aca ata ctg ata ttg tgc tca gta      102
82 Cys Val Ser Leu Trp Leu Leu Gly Thr Ile Leu Ile Leu Cys Ser Val
83   5          10          15          20
85 gac aac cac ggt ctg agg aga tgt ctg att tcc aca gac atg cac cat      150
86 Asp Asn His Gly Leu Arg Arg Cys Leu Ile Ser Thr Asp Met His His
87          25          30          35
89 ata gaa gag agt ttc caa gaa atc aaa aga gcc atc caa gct aag gac      198
90 Ile Glu Glu Ser Phe Gln Glu Ile Lys Arg Ala Ile Gln Ala Lys Asp
91          40          45          50
93 acc ttc cca aat gtc act atc ctg tcc aca ttg gag act ctg cag atc      246
94 Thr Phe Pro Asn Val Thr Ile Leu Ser Thr Leu Glu Thr Leu Gln Ile
95          55          60          65
97 att aag ccc tta gat gtg tgc tgc gtg acc aag aac ctc ctg gcg ttc      294
98 Ile Lys Pro Leu Asp Val Cys Cys Val Thr Lys Asn Leu Leu Ala Phe
99          70          75          80
101 tac gtg gac agg gtg ttc aag gat cat cag gag cca aac ccc aaa atc      342
102 Tyr Val Asp Arg Val Phe Lys Asp His Gln Glu Pro Asn Pro Lys Ile
103  85          90          95          100
105 ttg aga aaa atc agc agc att gcc aac tct ttc ctc tac atg cag aaa      390
106 Leu Arg Lys Ile Ser Ser Ile Ala Asn Ser Phe Leu Tyr Met Gln Lys
107          105          110          115
109 act ctg cgg caa tgt cag gaa cag agg cag tgt cac tgc agg cag gaa      438
110 Thr Leu Arg Gln Cys Gln Glu Gln Arg Gln Cys His Cys Arg Gln Glu
111          120          125          130
113 gcc acc aat gcc acc aga gtc atc cat gac aac tat gat cag ctg gag      486
114 Ala Thr Asn Ala Thr Arg Val Ile His Asp Asn Tyr Asp Gln Leu Glu
115          135          140          145
117 gtc cac gct gct gcc att aaa tcc ctg gga gag ctc gac gtc ttt cta      534
118 Val His Ala Ala Ala Ile Lys Ser Leu Gly Glu Leu Asp Val Phe Leu
119          150          155          160
121 gcc tgg att aat aag aat cat gaa gta atg tcc tca gct tgatgacaag      583
122 Ala Trp Ile Asn Lys Asn His Glu Val Met Ser Ser Ala
123 165          170          175
125 gaacctgtat agtgateccag ggatgaacac cccctgtgog gtttactgtg ggagacagcc 643
127 caccttgaag gggaaggaga tggggaaggc cccttgcagc tgaaagtccc actggctggc 703
129 ctcaggctgt cttattccgc ttgaaaatag ccaaaaagtc tactgtggta tttgtaataa 763
131 actctatctg ctgaaagggc ctgcaggcca tcctgggagt aaagggtgc cttcccatct 823
133 aatttattgt gaagtcatat agtccatgtc tgtgatgtga gccaaagtat atcctgtagt 883
135 acacattgta ctgagtgggt tttctgaata aattccatat ttacctatg aaaaaaaaaa 943
137 aaaaaaaaaa aaaccagctg agcgccggtc gctaccaag ccgaattc      991
140 <210> SEQ ID NO: 2

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141 <211> LENGTH: 177
142 <212> TYPE: PRT
143 <213> ORGANISM: Homo sapiens
145 <400> SEQUENCE: 2
146 Met Lys Leu Gln Cys Val Ser Leu Trp Leu Leu Gly Thr Ile Leu Ile
147   1           5           10           15
149 Leu Cys Ser Val Asp Asn His Gly Leu Arg Arg Cys Leu Ile Ser Thr
150           20           25           30
152 Asp Met His His Ile Glu Glu Ser Phe Gln Glu Ile Lys Arg Ala Ile
153           35           40           45
155 Gln Ala Lys Asp Thr Phe Pro Asn Val Thr Ile Leu Ser Thr Leu Glu
156           50           55           60
158 Thr Leu Gln Ile Ile Lys Pro Leu Asp Val Cys Cys Val Thr Lys Asn
159   65           70           75           80
161 Leu Leu Ala Phe Tyr Val Asp Arg Val Phe Lys Asp His Gln Glu Pro
162           85           90           95
164 Asn Pro Lys Ile Leu Arg Lys Ile Ser Ser Ile Ala Asn Ser Phe Leu
165           100          105          110
167 Tyr Met Gln Lys Thr Leu Arg Gln Cys Gln Glu Gln Arg Gln Cys His
168           115          120          125
170 Cys Arg Gln Glu Ala Thr Asn Ala Thr Arg Val Ile His Asp Asn Tyr
171           130          135          140
173 Asp Gln Leu Glu Val His Ala Ala Ala Ile Lys Ser Leu Gly Glu Leu
174 145           150          155          160
176 Asp Val Phe Leu Ala Trp Ile Asn Lys Asn His Glu Val Met Ser Ser
177           165          170          175
179 Ala
183 <210> SEQ ID NO: 3
184 <211> LENGTH: 531
185 <212> TYPE: DNA
186 <213> ORGANISM: Homo sapiens
188 <220> FEATURE:
189 <221> NAME/KEY: CDS
190 <222> LOCATION: (1)..(531)
192 <400> SEQUENCE: 3
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194 Met Lys Leu Gln Cys Val Ser Leu Trp Leu Leu Gly Thr Ile Leu Ile
195   1           5           10           15
197 ttg tgc tca gta gac aac cac ggt ctc agg aga tgt ctg att tcc aca   96
198 Leu Cys Ser Val Asp Asn His Gly Leu Arg Arg Cys Leu Ile Ser Thr
199           20           25           30
201 gac atg cac cat ata gaa gag agt ttc caa gaa atc aaa aga gcc atc   144
202 Asp Met His His Ile Glu Glu Ser Phe Gln Glu Ile Lys Arg Ala Ile
203           35           40           45
205 caa gct aag gac acc ttc cca aat gtc act atc ctg tcc aca ttg gag   192
206 Gln Ala Lys Asp Thr Phe Pro Asn Val Thr Ile Leu Ser Thr Leu Glu
207           50           55           60
209 act ctg cag atc att aag ccc tta gat gtg tgc tgc gtg acc aag aac   240
210 Thr Leu Gln Ile Ile Lys Pro Leu Asp Val Cys Cys Val Thr Lys Asn

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211 65          70          75          80
213 ctc ctg gcg ttc tac gtg gac agg gtg ttc aag gat cat cag gag cca 288
214 Leu Leu Ala Phe Tyr Val Asp Arg Val Phe Lys Asp His Gln Glu Pro
215          85          90          95
217 aac ccc aaa atc ttg aga aaa atc agc agc att gcc aac tct ttc ctc 336
218 Asn Pro Lys Ile Leu Arg Lys Ile Ser Ser Ile Ala Asn Ser Phe Leu
219          100          105          110
221 tac atg cag aaa act ctg cgg caa tgt cag gaa cag agg cag tgt cac 384
222 Tyr Met Gln Lys Thr Leu Arg Gln Cys Gln Glu Gln Arg Gln Cys His
223          115          120          125
225 tgc agg cag gaa gcc acc aat gcc acc aga gtc atc cat gac aac tat 432
226 Cys Arg Gln Glu Ala Thr Asn Ala Thr Arg Val Ile His Asp Asn Tyr
227          130          135          140
229 gat cag ctg gag gtc cac gct gct gcc att aaa tcc ctg gga gag ctc 480
230 Asp Gln Leu Glu Val His Ala Ala Ala Ile Lys Ser Leu Gly Glu Leu
231 145          150          155          160
233 gac gtc ttt cta gcc tgg att aat aag aat cat gaa gta atg tcc tca 528
234 Asp Val Phe Leu Ala Trp Ile Asn Lys Asn His Glu Val Met Ser Ser
235          165          170          175
237 gct 531
238 Ala
241 <210> SEQ ID NO: 4
242 <211> LENGTH: 153
243 <212> TYPE: PRT
244 <213> ORGANISM: Homo sapiens
246 <400> SEQUENCE: 4
247 Leu Arg Arg Cys Leu Ile Ser Thr Asp Met His His Ile Glu Glu Ser
248 1 5 10 15
250 Phe Gln Glu Ile Lys Arg Ala Ile Gln Ala Lys Asp Thr Phe Pro Asn
251 20 25 30
253 Val Thr Ile Leu Ser Thr Leu Glu Thr Leu Gln Ile Ile Lys Pro Leu
254 35 40 45
256 Asp Val Cys Cys Val Thr Lys Asn Leu Leu Ala Phe Tyr Val Asp Arg
257 50 55 60
259 Val Phe Lys Asp His Gln Glu Pro Asn Pro Lys Ile Leu Arg Lys Ile
260 65 70 75 80
262 Ser Ser Ile Ala Asn Ser Phe Leu Tyr Met Gln Lys Thr Leu Arg Gln
263 85 90 95
265 Cys Gln Glu Gln Arg Gln Cys His Cys Arg Gln Glu Ala Thr Asn Ala
266 100 105 110
268 Thr Arg Val Ile His Asp Asn Tyr Asp Gln Leu Glu Val His Ala Ala
269 115 120 125
271 Ala Ile Lys Ser Leu Gly Glu Leu Asp Val Phe Leu Ala Trp Ile Asn
272 130 135 140
274 Lys Asn His Glu Val Met Ser Ser Ala
275 145 150
278 <210> SEQ ID NO: 5
279 <211> LENGTH: 178
280 <212> TYPE: PRT

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381 <213> ORGANISM: Homo sapiens
383 <400> SEQUENCE: 5
384 Met His Ser Ser Ala Leu Leu Cys Cys Leu Val Leu Leu Thr Gly Val
385 1 5 10 15
387 Arg Ala Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His
388 20 25 30
390 Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe
391 35 40 45
393 Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu
394 50 55 60
396 Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys
397 65 70 75 80
399 Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro
400 85 90 95
402 Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu
403 100 105 110
405 Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg
406 115 120 125
408 Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn
409 130 135 140
411 Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu
412 145 150 155 160
414 Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile
415 165 170 175
417 Arg Asn
421 <210> SEQ ID NO: 6
422 <211> LENGTH: 178
423 <212> TYPE: PRT
424 <213> ORGANISM: Artificial Sequence
426 <220> FEATURE:
427 <223> OTHER INFORMATION: Description of Artificial Sequence: Mus musculus
429 <400> SEQUENCE: 6
430 Met Pro Gly Ser Ala Leu Leu Cys Cys Leu Leu Leu Leu Thr Gly Met
431 1 5 10 15
433 Arg Ile Ser Arg Gly Gln Tyr Ser Arg Glu Asp Asn Asn Cys Thr His
434 20 25 30
436 Phe Pro Val Gly Gln Ser His Met Leu Leu Glu Leu Arg Thr Ala Phe
437 35 40 45
439 Ser Gln Val Lys Thr Phe Phe Gln Thr Lys Asp Gln Leu Asp Asn Ile
440 50 55 60
442 Leu Leu Thr Asp Ser Leu Met Gln Asp Phe Lys Gly Tyr Leu Gly Cys
443 65 70 75 80
445 Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Val Glu Val Met Pro
446 85 90 95
448 Gln Ala Glu Lys His Gly Pro Glu Ile Lys Glu His Leu Asn Ser Leu
449 100 105 110
451 Gly Glu Lys Leu Lys Thr Leu Arg Met Arg Leu Arg Arg Cys His Arg
452 115 120 125
454 Phe Leu Lys Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Ser

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fyi

Please Note:

Use f n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
 PATENT APPLICATION: US/09/782,980

DATE: 03/12/2001
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Input Set : A:\seqlist.txt
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L:18 M:270 C: Current Application Number differs, Replaced Application Number
 L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:1088 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
 L:1088 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
 L:1088 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:13
 L:1091 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
 L:1091 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
 M:340 Repeated in SeqNo=13
 L:1094 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
 L:1094 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
 L:2868 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:42
 L:2868 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:42
 L:2868 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:42
 L:4587 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:63
 L:4587 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:63
 L:4587 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:63
 L:4590 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:63
 L:4590 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:63
 M:340 Repeated in SeqNo=63
 L:4611 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:64
 L:4611 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:64
 L:4611 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:64
 L:4614 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:64
 L:4614 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:64
 M:340 Repeated in SeqNo=64
 L:4617 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:64
 L:4617 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:64
 L:4639 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:65
 L:4639 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:65
 L:4639 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:65
 L:4642 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:65
 L:4642 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:65
 M:340 Repeated in SeqNo=65
 L:4645 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:65
 L:4645 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:65
 L:6061 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:76
 L:6061 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:76
 L:6061 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:76
 L:6064 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:76
 L:6064 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:76
 M:340 Repeated in SeqNo=76
 L:6116 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:77
 L:6116 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:77
 L:6116 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:77
 L:7273 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:127
 L:7273 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:127
 L:7273 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:127
 L:7307 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:128

VERIFICATION SUMMARY DATE: 03/12/2001
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Input Set : A:\seqlist.txt
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L:7307 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:128
L:7307 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:128
L:7336 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:129
L:7336 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:129
L:7336 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:129
L:7339 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:129
L:7339 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:129
M:340 Repeated in SeqNo=129
L:8081 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:176
L:8081 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:176
L:8081 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:176